

Seq1: Hi-AF (104 mers)

5'-gatcctttatggttggttacactgactgcactgaatccggtcagaaacctgtgcctgtg
cgaaggctctaacggttgccggccagggaacaaatgcatacctgggc-3'

Seq2: Hi-AR (107 mers)

5'-ctctagagcccaggatgcatttggtgccctggccgcaaacgtagagccttcgcacag
gcacagggtctgaccggattcagtcagtcagtgtaaacacaccataaag-3'

Seq3: Hi-BF (111 mers)

5'-tctagaggcgaaaaaatcaatgcgttactggcggaagggtactccacaaggcttgaat
cccgggaagaatagaaacccgcagtcctccgacgacagaacctgcaataatagggc-3'

Seq4: Hi-BF (108 mers)

5'-ggccgccctattatgcagggtattcttcgggatttctcaaatgctgccgctcgttg
agactgcgggttcggagtaccttcgccagtaacgcattgattttttcgc-3'

Figure 1

105364.00102

Seq5: Hi-PCR-AF (33 mers)
5'-tcgggatcctttatggttgtttacactgactgc-3'

Seq6: Hi-PCR-AR (31 mers)
5'-gcctctagagagccaggatgcatttggtgcc-3'

Seq7: Hi-PCR-BF (38 mers)
5'-ggctctagaggcgaaaaaatcaatgcgttactggcga-3'

Seq8: Hi-PCR-BR (32 mers)
5'-catgcggccgccctattattgcaggtattctt-3'

Figure 2

10053641.054402

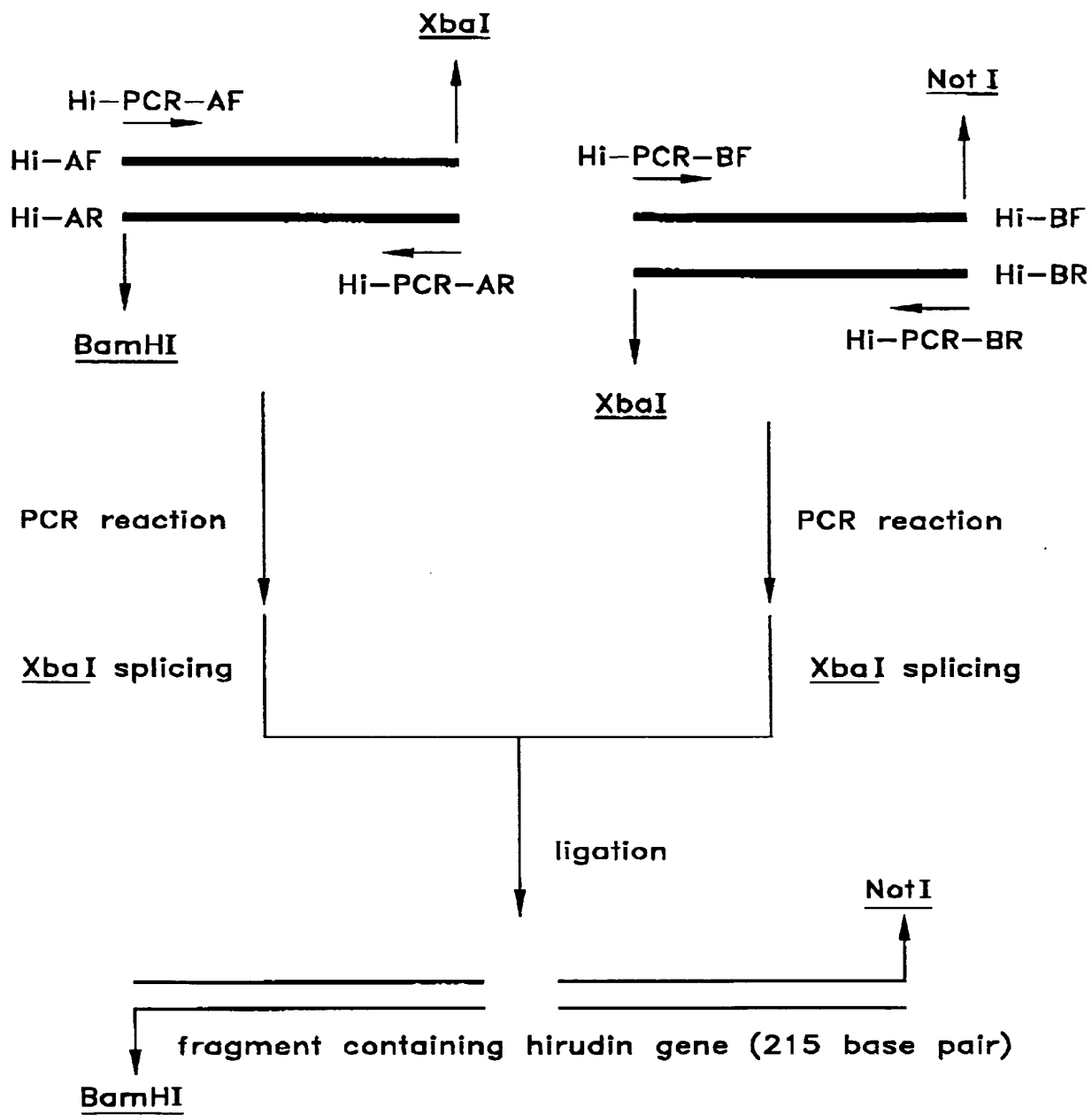


Figure 3

(A)

GATCCTTT ATG GTT GTT TAC ACT GAC TGC ACT GAA TCC GGT CAG
AAC CTG TGC CTG TGC GAA GGC TCT AAC GTT TGC GGC CAG GGC
AAC AAA TGC ATC CTG GGC TCT AGA GGC GAA AAA AAC CAG TGC
GTT ACT GGC GAA GGT ACC CCG AAA CCG CAG TCT CAC AAC GAC
GGC GAC TTC GAA GAA ATC CCG GAA GAA TAC CTG CAG TAA TAGGGC

(B)

Met Val Val Tyr Thr Asp Cys Thr Glu Ser Gly Gln Asn Leu
Cys Leu Cys Glu Gly Ser Asn Val Cys Gly Gln Gly Asn Lys
Cys Ile Leu Gly Ser Arg Gly Glu Lys Asn Gln Cys Val Thr
Gly Glu Gly Thr Pro Lys Pro Gln Ser His Asn Asp Gly Asp
Phe Glu Glu Ile Pro Glu Glu Tyr Leu Gln

Figure 4

204T50" T49E500T

5/8

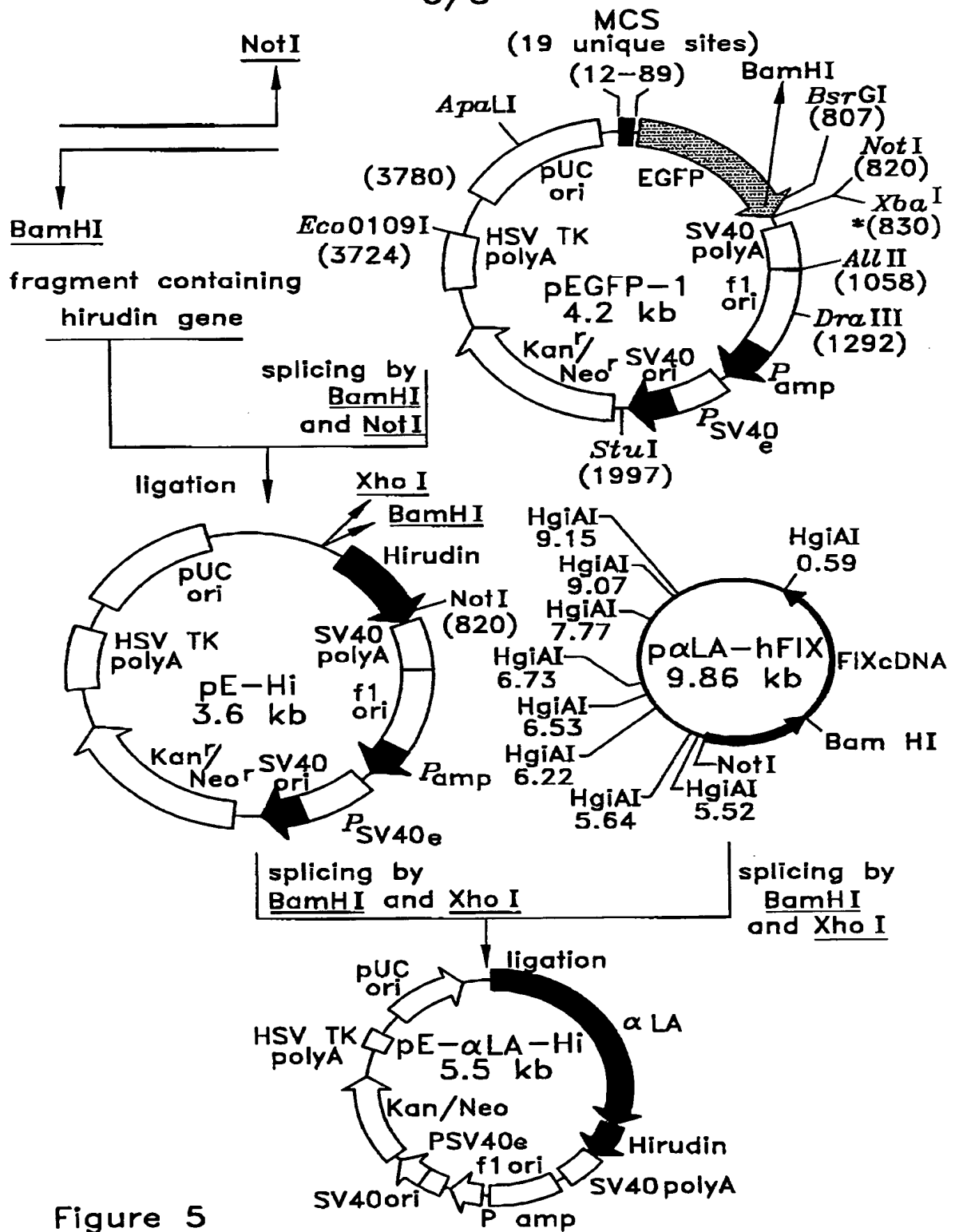


Figure 5

20053644.051402

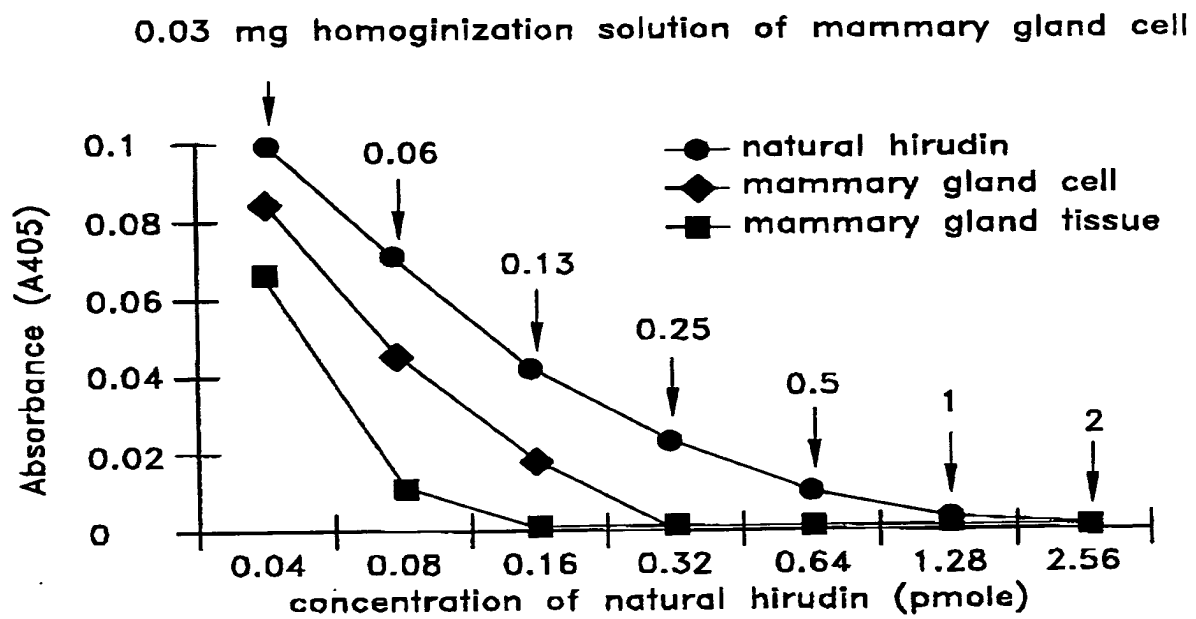


Figure 6

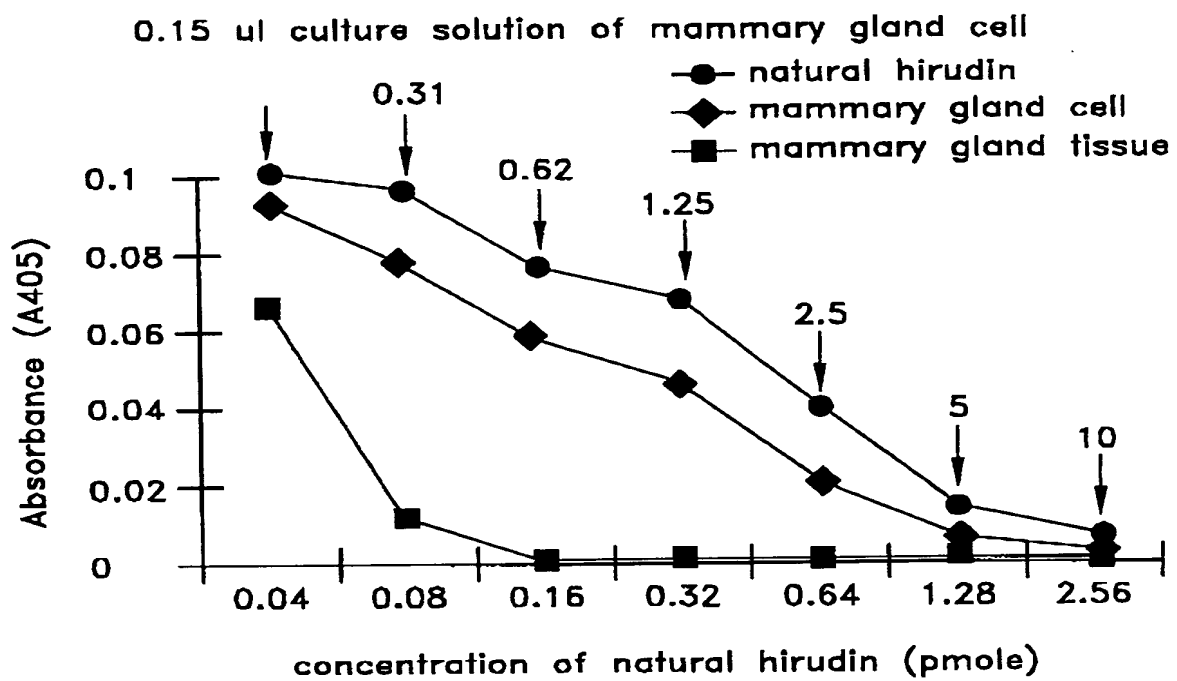
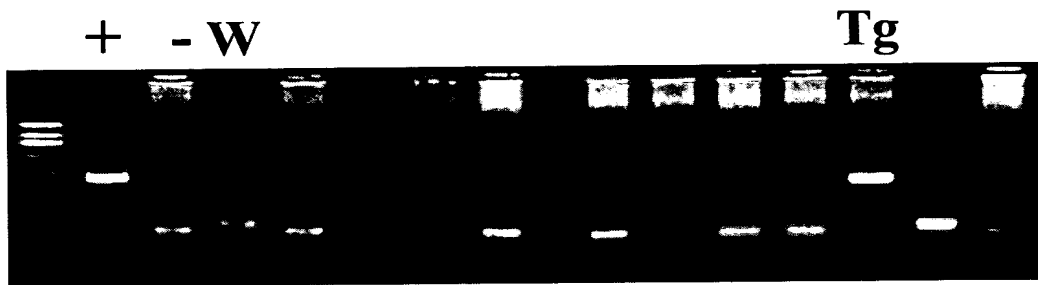


Figure 7

(A)



(B)

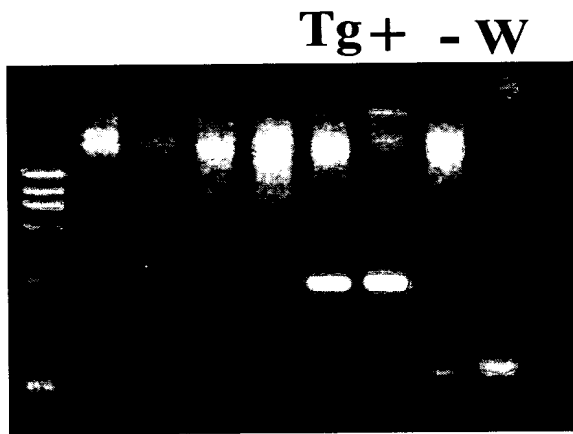


Fig. 8

4.0003641.054402